

SEQUENCE LISTING

<110> Wolfraim, Lawrence
Letterio, John

<120> FUNCTIONALIZED TGF-BETA FUSION PROTEINS

<130> 4239-61302

<150> 60/242,292

<151> 2000-10-20

<160> 39

<170> PatentIn version 3.1

<210> 1

<211> 28

<212> DNA

<213> synthetic oligonucleotide

<400> 1

ggagagatct ggtaccgaga tggcgctt

28

<210> 2

<211> 42

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<213> synthetic oligonucleotide

<400> 2

ataagaattg cggccgttt aatogatccc aagtgggctt gg

42

<210> 3

<211> 48

<212> DNA

<213> synthetic oligonucleotide

<400> 3

gactacaagg atgacgacga caaggccctg gataccaact actgcttc

48

<210> 4

<211> 45

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<213> synthetic oligonucleotide

<400> 4

cttgctgctg tcatccttgt agtctcggcg gtgccgggag ctgtg

45

<210> 5

<211> 45

<212> DNA

<213> synthetic oligonucleotide

<400> 5

gactacaagg atgacgacga caggagaaga actgctgcgt gcggc

45

<210> 6
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 <213> synthetic oligonucleotide

<400> 6
 cttgtcgtcg tcataccttgt agtctcggcg gtgccgggag ctgtg

45

<210> 7
 <211> 8
 <212> PRT
 <213> synthetic oligopeptide

<400> 7

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 8
 <211> 1197
 <212> DNA
 <213> fusion

<220>
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 <222> (1)..(1197)
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 <222> (278)..(279)
 <223> Maturation cleavage site

<400> 8
 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg
 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
 1 5 10 15

48

tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc
 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

96

tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc
 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

144

att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc
 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

192

cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt
 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

240

tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag
 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95

288

atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac 1056
Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
340 345 350

cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg 1104
Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
355 360 365

ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg 1152
Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
370 375 380

gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga 1197
Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
385 390 395

<210> 9

<211> 398

<212> PRT

<213> fusion

<220>

<221> misc_feature

<222> (278)..(279)

<223> Maturation cleavage site

<400> 9

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
 210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
 225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
 275 280 285

Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
 290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
 305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
 325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
 340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
 355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 385 390 395

<210> 10
 <211> 362
 <212> DNA
 <213> fusion

<400> 10
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 aagaactgct gcgtgcggca gctctacatt gacttcggga aggacctggg ctggaagtgg 120
 attcatgaac ccaagggctc catgccaaatt tctgcctggg gccctgtccc tacatctgga 180
 gcctagacac tcagtacagc aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcggt 240
 cggcgggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcgtg tactacgtgg 300
 gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttcctgc aagtgcagct 360
 ga 362

<210> 11
 <211> 120
 <212> PRT
 <213> fusionprotein

<220>
 <221> PEPTIDE
 <222> (1)..(8)
 <223> FLAG tag

<400> 11

Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe
 1 5 10 15

Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
 20 25 30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
 35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
 50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
 65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
115 120

<210> 12
<211> 1197
<212> DNA
<213> fusion

<220>
<221> CDS
<222> (1)..(1197)
<223>

<220>
<221> misc_feature
<222> (278)..(279)
<223> Maturation cleavage site

<400> 12
atg gcg cct tgc ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg 48
Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15
tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc 96
Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30
tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45
att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192
Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60
cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt 240
Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80
tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag 288
Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95
ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta 336
Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110
atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc 384
Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val 130 135 140	432
ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu 145 150 155 160	480
aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn 165 170 175	528
gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser 180 185 190	576
ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu 195 200 205	624
acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser 210 215 220	672
tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn 225 230 235 240	720
tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro 245 250 255	768
ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His 260 265 270	816
agc tcc cgg cac cgc cga gcc ctg gat acc aac tac tgc ttc agc tcc Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser 275 280 285	864
acg gac tac aag gat gac gac gac aag gag aag aac tgc tgc gtg cgg Thr Asp Tyr Lys Asp Asp Asp Asp Lys Glu Lys Asn Cys Cys Val Arg 290 295 300	912
cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His 305 310 315 320	960
gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr 325 330 335	1008
atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn 340 345 350	1056
cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala 355 360 365	1104

ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg 1152
 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
 370 375 380

gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga 1197
 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 385 390 395

<210> 13
 <211> 398
 <212> PRT
 <213> fusion

<220>
 <221> misc_feature
 <222> (278)..(279)
 <223> Maturation cleavage site

<400> 13

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
 1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

<211> 362
 <212> DNA
 <213> fusion

<400> 14
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 aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctggaagtgg 120
 attcatgaac ccaagggcta ccattgccaat ttctgcctgg ggccctgtcc ctacatctgg 180
 agcctagaca ctcagtacac aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt 240
 cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcgtg tactacgtgg 300
 gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttcctgc aagtgcagct 360
 ga 362

<210> 15
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 <212> PRT
 <213> fusionprotein

<220>
 <221> peptide
 <222> (12)..(19)
 <223> FLAG tag

<400> 15

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Asp Tyr Lys Asp Asp
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Asp Asp Lys Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
 20 25 30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
 35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
 50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
 65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
 85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
 100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
115 120

<210> 16
<211> 1612
<212> DNA
<213> Fusion

<220>
<221> CDS
<222> (348)..(1559)
<223>

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<221> 5'UTR
<222> (1)..(347)
<223>

<220>
<221> 3'UTR
<222> (1560)..(1612)
<223>

<220>
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<222> (1182)..(1196)
<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
<221> misc_feature
<222> (1197)..(1220)
<223> Encodes FLAG epitope tag

<220>
<221> misc_feature
<222> (1182)..(1159)
<223> Encodes ature fusion protein

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agagcgctca tctcgatttt taccctgggtg gtatactgag acaccttggt gtcagagcct 180
caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct 240
ttccttggga gacccacccc cacaagccct gcagggggcgg ggcctcogca tcccaccttt 300
gccgagggtt cccgctctcc gaagtgccgt ggggcgcgcg ctcccc atg ccg ccc 356
Met Pro Pro
1
tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta 404

Ser	Gly	Leu	Arg	Leu	Leu	Pro	Leu	Leu	Leu	Pro	Leu	Pro	Trp	Leu	Leu		
5						10					15						
gtg	ctg	acg	ccc	ggg	agg	cca	gcc	gcg	gga	ctc	tcc	acc	tgc	aag	acc	452	
Val	Leu	Thr	Pro	Gly	Arg	Pro	Ala	Ala	Gly	Leu	Ser	Thr	Cys	Lys	Thr	35	
20					25					30							
atc	gac	atg	gag	ctg	gtg	aaa	cgg	aag	cgc	atc	gaa	gcc	atc	cgt	ggc	500	
Ile	Asp	Met	Glu	Leu	Val	Lys	Arg	Lys	Arg	Ile	Glu	Ala	Ile	Arg	Gly	50	
				40					45								
cag	atc	ctg	tcc	aaa	cta	agg	ctc	gcc	agt	ccc	cca	agc	cag	ggg	gag	548	
Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Ala	Ser	Pro	Pro	Ser	Gln	Gly	Glu	65	
			55					60									
gta	ccg	ccc	ggc	ccg	ctg	ccc	gag	gcg	gtg	ctc	gct	ttg	tac	aac	agc	596	
Val	Pro	Pro	Gly	Pro	Leu	Pro	Glu	Ala	Val	Leu	Ala	Leu	Tyr	Asn	Ser	80	
			70				75										
acc	cgc	gac	cgg	gtg	gca	ggc	gag	agc	gcc	gac	cca	gag	ccg	gag	ccc	644	
Thr	Arg	Asp	Arg	Val	Ala	Gly	Glu	Ser	Ala	Asp	Pro	Glu	Pro	Glu	Pro	95	
	85					90											
gaa	gcg	gac	tac	tat	gct	aaa	gag	gtc	acc	cgc	gtg	cta	atg	gtg	gac	692	
Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr	Arg	Val	Leu	Met	Val	Asp	115	
100					105					110							
cgc	aac	aac	gcc	atc	tat	gag	aaa	acc	aaa	gac	atc	tca	cac	agt	ata	740	
Arg	Asn	Asn	Ala	Ile	Tyr	Glu	Lys	Thr	Lys	Asp	Ile	Ser	His	Ser	Ile	130	
				120					125								
tat	atg	ttc	ttc	aat	acg	tca	gac	att	cgg	gaa	gca	gtg	ccc	gaa	ccc	788	
Tyr	Met	Phe	Phe	Asn	Thr	Ser	Asp	Ile	Arg	Glu	Ala	Val	Pro	Glu	Pro	145	
			135					140									
cca	ttg	ctg	tcc	cgt	gca	gag	ctg	cgc	ttg	cag	aga	tta	aaa	tca	agt	836	
Pro	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu	Gln	Arg	Leu	Lys	Ser	Ser	160	
			150				155										
gtg	gag	caa	cat	gtg	gaa	ctc	tac	cag	aaa	tat	agc	aac	aat	tcc	tgg	884	
Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys	Tyr	Ser	Asn	Asn	Ser	Trp	175	
			165			170											
cgt	tac	ctt	ggt	aac	cgg	ctg	ctg	acc	ccc	act	gat	acg	cct	gag	tgg	932	
Arg	Tyr	Leu	Gly	Asn	Arg	Leu	Leu	Thr	Pro	Thr	Asp	Thr	Pro	Glu	Trp	195	
180					185					190							
ctg	tct	ttt	gac	gtc	act	gga	gtt	gta	cgg	cag	tgg	ctg	aac	caa	gga	980	
Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg	Gln	Trp	Leu	Asn	Gln	Gly	210	
				200					205								
gac	gga	ata	cag	ggc	ttt	cga	ttc	agc	gct	cac	tgc	tct	tgt	gac	agc	1028	
Asp	Gly	Ile	Gln	Gly	Phe	Arg	Phe	Ser	Ala	His	Cys	Ser	Cys	Asp	Ser	225	
			215					220									
aaa	gat	aac	aaa	ctc	cac	gtg	gaa	atc	aac	ggg	atc	agc	ccc	aaa	cgt	1076	
Lys	Asp	Asn	Lys	Leu	His	Val	Glu	Ile	Asn	Gly	Ile	Ser	Pro	Lys	Arg	240	
			230				235										
cgg	ggc	gac	ctg	ggc	acc	atc	cat	gac	atg	aac	cgg	ccc	ttc	ctg	ctc	1124	
Arg	Gly	Asp	Leu	Gly	Thr	Ile	His	Asp	Met	Asn	Arg	Pro	Phe	Leu	Leu		

245	250	255	
ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg			1172
Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg			
260	265	270	275
cac cgg aga gcc ctg gat acc aac gac tac aag gat gac gac gac aag			1220
His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp Asp Asp Lys			
	280	285	290
gcc ctg gat acc aac tat tgc ttc agc tcc aca gag aag aac tgc tgt			1268
Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys			
	295	300	305
gtg cgg cag ctg tac att gac ttt agg aag gac ctg ggt tgg aag tgg			1316
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp			
	310	315	320
atc cac gag ccc aag ggc tac cat gcc aac ttc tgt ctg gga ccc tgc			1364
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys			
	325	330	335
ccc tat att tgg agc ctg gac aca cag tac agc aag gtc ctt gcc ctc			1412
Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu			
	340	345	350
tac aac caa cac aac ccg ggc gct tcg gcg tca ccg tgc tgc gtg ccg			1460
Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys Cys Val Pro			
	360	365	370
cag gct ttg gag cca ctg ccc atc gtc tac tac gtg ggt cgc aag ccc			1508
Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro			
	375	380	385
aag gtg gag cag ttg tcc aac atg att gtg cgc tcc tgc aag tgc agc			1556
Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser			
	390	395	400
tga agccccgccc cgccccgccc ctccccggcag gcccgcccc gccccccgccc cgc			1612

<210> 17
 <211> 403
 <212> PRT
 <213> Fusion

<220>
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 <222> (1182)..(1196)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (1197)..(1220)
 <223> Encodes FLAG epitope tag

<220>
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 <223> Encodes ature fusion protein

<400> 17

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
 275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys
 355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 385 390 395 400

Lys Cys Ser

<210> 18
 <211> 73
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<220>
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 ttcagctcca cgg 73

<210> 19
 <211> 72

<212> DNA
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<400> 19
 cttgtcgtcg tcatccttgt agtcgttata cagggctcgg cggtggtgcc gggagctgtg 60
 caggtgctgg gc 72

<210> 20
 <211> 1624
 <212> DNA
 <213> Fusion

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 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (1197)..(1232)
 <223> Encodes HA epitope tag

<220>
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 <222> (1182)..(1571)
 <223> Encodes mature fusion protein

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 ctccctcgga cctgctggca gtagctcccc tatttaagaa caccacttt tggatctcag 120
 agagcgctca tctcgatttt taccctgggt gtatactgag acaccttggt gtcagagcct 180
 caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct 240

ttccttgga gacccacccc cacaagccct gcagggcgcg ggccctccgca tcccaccttt	300
gccgaggggtt cccgctctcc gaagtgccgt ggggcgcgcg ccccc atg ccg ccc	356
Met Pro Pro	
1	
tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta	404
Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro Trp Leu Leu	
5 10 15	
gtg ctg acg ccc ggg agg cca gcc gcg gga ctc tcc acc tgc aag acc	452
Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr	
20 25 30 35	
atc gac atg gag ctg gtg aaa cgg aag cgc atc gaa gcc atc cgt ggc	500
Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly	
40 45 50	
cag atc ctg tcc aaa cta agg ctc gcc agt ccc cca agc cag ggg gag	548
Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu	
55 60 65	
gta ccg ccc ggc ccg ctg ccc gag gcg gtg ctc gct ttg tac aac agc	596
Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser	
70 75 80	
acc cgc gac cgg gtg gca ggc gag agc gcc gac cca gag ccg gag ccc	644
Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro	
85 90 95	
gaa gcg gac tac tat gct aaa gag gtc acc cgc gtg cta atg gtg gac	692
Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp	
100 105 110 115	
cgc aac aac gcc atc tat gag aaa acc aaa gac atc tca cac agt ata	740
Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile	
120 125 130	
tat atg ttc ttc aat acg tca gac att cgg gaa gca gtg ccc gaa ccc	788
Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro	
135 140 145	
cca ttg ctg tcc cgt gca gag ctg cgc ttg cag aga tta aaa tca agt	836
Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser	
150 155 160	
gtg gag caa cat gtg gaa ctc tac cag aaa tat agc aac aat tcc tgg	884
Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp	
165 170 175	
cgt tac ctt ggt aac cgg ctg ctg acc ccc act gat acg cct gag tgg	932
Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp	
180 185 190 195	
ctg tct ttt gac gtc act gga gtt gta cgg cag tgg ctg aac caa gga	980
Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly	
200 205 210	
gac gga ata cag ggc ttt cga ttc agc gct cac tgc tct tgt gac agc	1028
Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser	

215	220	225	
aaa gat aac aaa ctc cac gtg gaa atc aac ggg atc agc ccc aaa cgt			1076
Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg			
230	235	240	
cgg ggc gac ctg ggc acc atc cat gac atg aac cgg ccc ttc ctg ctc			1124
Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu			
245	250	255	
ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg			1172
Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg			
260	265	270	275
cac cgg aga gcc ctg gat acc aac agc tac cca tac gac gtg cca gac			1220
His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp Val Pro Asp			
280	285	290	
tac gca tct ctg gcc ctg gat acc aac tat tgc ttc agc tcc aca gag			1268
Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu			
295	300	305	
aag aac tgc tgt gtg cgg cag ctg tac att gac ttt agg aag gac ctg			1316
Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu			
310	315	320	
ggg tgg aag tgg atc cac gag ccc aag ggc tac cat gcc aac ttc tgt			1364
Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys			
325	330	335	
ctg gga ccc tgc ccc tat att tgg agc ctg gac aca cag tac agc aag			1412
Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys			
340	345	350	355
gtc ctt gcc ctc tac aac caa cac aac ccg ggc gct tcg gcg tca ccg			1460
Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro			
360	365	370	
tgc tgc gtg ccg cag gct ttg gag cca ctg ccc atc gtc tac tac gtg			1508
Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val			
375	380	385	
ggg cgc aag ccc aag gtg gag cag ttg tcc aac atg att gtg cgc tcc			1556
Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser			
390	395	400	
tgc aag tgc agc tga agccccgccc cgccccgccc ctccccggcag gcccgcccc			1611
Cys Lys Cys Ser			
405			
gcccccgccc cgc			1624

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 <211> 407
 <212> PRT
 <213> Fusion

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 <222> (1182)..(1196)

<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>

<221> misc_feature

<222> (1197)..(1232)

<223> Encodes HA epitope tag

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<221> misc_feature

<222> (1182)..(1571)

<223> Encodes mature fusion protein

<400> 21

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
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<210> 22
<211> 108
<212> DNA
<213> artificial sequence

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gccctggata ccaacagcta cccatacgac gtgccagact acgcatctct ggcctggat      60

accaactact gcttcagctc cacggagaag aactgctgcg tgcggcag                    108

<210> 23
<211> 73
<212> DNA
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<220>
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<400> 23
cagagatgcg tagtctggca cgtcgtatgg gtagctgttg gtagccaggg ctgggcggtg      60

ccgggagctg tgc                                                            73

<210> 24
<211> 1284
<212> DNA
<213> Fusion

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<222> (1)..(1284)
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<222> (907)..(921)
<223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
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<222> (922)..(945)
<223> Encodes FLAG epitope tag

<220>
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<222> (907)..(1284)
<223> Encodes mature fusion protein

<400> 24
atg cac tac tgt gtg ctg agc acc ttt ttg ctc ctg cat ctg gtc ccg      48
Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
1          5          10          15

gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat cag ttt      96
Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
          20          25          30

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atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc aag ctg	144
Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu	
35 40 45	
aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag gtc ccc	192
Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro	
50 55 60	
ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg cag gag	240
Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu	
65 70 75 80	
aag gca agc cgg agg gca gcc gcc tgc gag cgc gag cgg agc gag cag	288
Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln	
85 90 95	
gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc cac ctc	336
Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu	
100 105 110	
ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac ttc aga	384
Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg	
115 120 125	
atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tgc aat ctg	432
Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu	
130 135 140	
gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa gcc aga	480
Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg	
145 150 155 160	
gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc aaa gac	528
Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp	
165 170 175	
tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg aaa acc	576
Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr	
180 185 190	
aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct gtg cag	624
Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln	
195 200 205	
gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata agt tta	672
Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu	
210 215 220	
cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc atc ccg	720
His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro	
225 230 235 240	
aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat ggc acc	768
Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr	
245 250 255	
tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act agg aaa	816
Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys	
260 265 270	

aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg ccc tcc	864
Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser	
275 280 285	
tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc gct ttg	912
Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu	
290 295 300	
gat gct gcc gac tac aag gat gac gac gac aag gct ttg gat gct gcc	960
Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala	
305 310 315 320	
tac tgc ttt aga aat gtg cag gat aat tgc tgc ctt cgc cct ctt tac	1008
Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr	
325 330 335	
att gat ttt aag agg gat ctt gga tgg aaa tgg atc cat gaa ccc aaa	1056
Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys	
340 345 350	
ggg tac aat gct aac ttc tgt gct ggg gca tgc cca tat cta tgg agt	1104
Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser	
355 360 365	
tca gac act caa cac acc aaa gtc ctc agc ctg tac aac acc ata aat	1152
Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn	
370 375 380	
ccc gaa gct tcc gct tcc cct tgc tgt gtg tcc cag gat ctg gaa cca	1200
Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro	
385 390 395 400	
ctg acc att ctc tat tac att gga aat acg ccc aag atc gaa cag ctt	1248
Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu	
405 410 415	
tcc aat atg att gtc aag tct tgt aaa tgc agc taa	1284
Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser	
420 425	

<210> 25
 <211> 427
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 <213> Fusion

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 <223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
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 <222> (922)..(945)
 <223> Encodes FLAG epitope tag

<220>
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 <222> (907)..(1284)
 <223> Encodes mature fusion protein

<400> 25

Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
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Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
115 120 125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145 150 155 160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala
305 310 315 320

Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr
325 330 335

Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys
340 345 350

Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser
355 360 365

Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn
370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro
385 390 395 400

Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu
405 410 415

Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
420 425

<210> 26
<211> 1303
<212> DNA
<213> Fusion

<220>
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<220>

<221> 5'UTR
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 <222> (929)..(964)
 <223> Encodes HA epitope tag

<220>
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 <222> (914)..(1303)
 <223> Encodes mature fusion protein

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 1 5 10

gtc ccg gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat 97
 Val Pro Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp
 15 20 25 30

cag ttt atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc 145
 Gln Phe Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser
 35 40 45

aag ctg aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag 193
 Lys Leu Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu
 50 55 60

gtc ccc ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg 241
 Val Pro Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu
 65 70 75

cag gag aag gca agc cgg agg gca gcc gcc tgc gag cgc gag cgg agc 289
 Gln Glu Lys Ala Ser Arg Arg Ala Ala Cys Glu Arg Glu Arg Ser
 80 85 90

gag cag gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc 337
 Glu Gln Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser
 95 100 105 110

cac ctc ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac 385
 His Leu Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr
 115 120 125

ttc aga atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tcg 433
 Phe Arg Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser
 130 135 140

aat ctg gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa 481

Asn	Leu	Val	Lys	Ala	Glu	Phe	Arg	Val	Phe	Arg	Leu	Gln	Asn	Pro	Lys		
		145					150					155					
gcc	aga	gtg	gcc	gag	cag	cgg	att	gaa	ctg	tat	cag	atc	ctt	aaa	tcc		529
Ala	Arg	Val	Ala	Glu	Gln	Arg	Ile	Glu	Leu	Tyr	Gln	Ile	Leu	Lys	Ser		
		160					165				170						
aaa	gac	tta	aca	tct	ccc	acc	cag	cgc	tac	atc	gat	agc	aag	gtt	gtg		577
Lys	Asp	Leu	Thr	Ser	Pro	Thr	Gln	Arg	Tyr	Ile	Asp	Ser	Lys	Val	Val		
		175				180				185					190		
aaa	acc	aga	gcg	gag	ggg	gaa	tgg	ctc	tcc	ttc	gac	gtg	aca	gac	gct		625
Lys	Thr	Arg	Ala	Glu	Gly	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Asp	Ala		
				195					200					205			
gtg	cag	gag	tgg	ctt	cac	cac	aaa	gac	agg	aac	ctg	ggg	ttt	aaa	ata		673
Val	Gln	Glu	Trp	Leu	His	His	Lys	Asp	Arg	Asn	Leu	Gly	Phe	Lys	Ile		
			210					215					220				
agt	tta	cac	tgc	ccc	tgc	tgt	acc	ttc	gtg	cgc	tct	aat	aat	tac	atc		721
Ser	Leu	His	Cys	Pro	Cys	Cys	Thr	Phe	Val	Pro	Ser	Asn	Asn	Tyr	Ile		
		225					230					235					
atc	ccg	aat	aaa	agc	gaa	gag	ctc	gag	gcg	aga	ttt	gca	ggg	att	gat		769
Ile	Pro	Asn	Lys	Ser	Glu	Glu	Leu	Glu	Ala	Arg	Phe	Ala	Gly	Ile	Asp		
		240				245					250						
ggc	acc	tct	aca	tat	gcc	agt	ggg	gat	cag	aaa	act	ata	aag	tcc	act		817
Gly	Thr	Ser	Thr	Tyr	Ala	Ser	Gly	Asp	Gln	Lys	Thr	Ile	Lys	Ser	Thr		
		255			260					265					270		
agg	aaa	aaa	acc	agt	ggg	aag	acc	cca	cat	ctc	ctg	cta	atg	ttg	ttg		865
Arg	Lys	Lys	Thr	Ser	Gly	Lys	Thr	Pro	His	Leu	Leu	Leu	Met	Leu	Leu		
				275				280						285			
ccc	tcc	tac	aga	ctg	gag	tca	caa	cag	tcc	agc	cgg	cgg	aag	aag	cgc		913
Pro	Ser	Tyr	Arg	Leu	Glu	Ser	Gln	Gln	Ser	Ser	Arg	Arg	Lys	Lys	Arg		
			290					295					300				
gct	ttg	gat	gct	gcc	agc	tac	cca	tac	gac	gtg	cca	gac	tac	gca	tct		961
Ala	Leu	Asp	Ala	Ala	Ser	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser		
		305					310					315					
ctg	gct	ttg	gat	gct	gcc	tac	tgc	ttt	aga	aat	gtg	cag	gat	aat	tgc		1009
Leu	Ala	Leu	Asp	Ala	Ala	Tyr	Cys	Phe	Arg	Asn	Val	Gln	Asp	Asn	Cys		
		320				325					330						
tgc	ctt	cgc	cct	ctt	tac	att	gat	ttt	aag	agg	gat	ctt	gga	tgg	aaa		1057
Cys	Leu	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Lys	Arg	Asp	Leu	Gly	Trp	Lys		
		335			340				345						350		
tgg	atc	cat	gaa	ccc	aaa	ggg	tac	aat	gct	aac	ttc	tgt	gct	ggg	gca		1105
Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	Asn	Ala	Asn	Phe	Cys	Ala	Gly	Ala		
				355				360						365			
tgc	cca	tat	cta	tgg	agt	tca	gac	act	caa	cac	acc	aaa	gtc	ctc	agc		1153
Cys	Pro	Tyr	Leu	Trp	Ser	Ser	Asp	Thr	Gln	His	Thr	Lys	Val	Leu	Ser		
			370					375					380				
ctg	tac	aac	acc	ata	aat	ccc	gaa	gct	tcc	gct	tcc	cct	tgc	tgt	gtg		1201
Leu	Tyr	Asn	Thr	Ile	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val		

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
 100 105 110
 Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
 115 120 125
 Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
 130 135 140
 Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
 145 150 155 160
 Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
 165 170 175
 Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
 180 185 190
 Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
 195 200 205
 Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
 210 215 220
 His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
 225 230 235 240
 Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
 245 250 255
 Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
 260 265 270
 Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
 275 280 285
 Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
 290 295 300
 Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala
 305 310 315 320
 Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu
 325 330 335
 Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile

340

345

350

His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro
 355 360 365

Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr
 370 375 380

Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln
 385 390 395 400

Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys
 405 410 415

Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
 420 425 430

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 <213> Fusion

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 <223> Encodes FLAG epitope tag

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 Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
 1 5 10 15

aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac 96
 Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
 20 25 30

atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys 35 40 45	144
ctc agg ctc acc agc ccc cct gag cca tgc gtg atg acc cac gtc ccc Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro 50 55 60	192
tat cag gtc ctg gca ctt tac aac agc acc cgg gag ttg ctg gaa gag Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu 65 70 75 80	240
atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tgc gag tct Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser 85 90 95	288
gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu 100 105 110	336
gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys 115 120 125	384
gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu 130 135 140	432
ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys 145 150 155 160	480
cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu 165 170 175	528
cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg 180 185 190	576
ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu 195 200 205	624
tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His 210 215 220	672
tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val 225 230 235 240	720
cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp 245 250 255	768
cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His 260 265 270	816
aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc	864

Asn	Pro	His	Leu	Ile	Leu	Met	Met	Ile	Pro	Pro	His	Arg	Leu	Asp	Ser		
		275					280					285					
cca	ggc	cag	ggc	agt	cag	agg	aag	aag	agg	gcc	ctg	gac	acc	aat	gac	912	
Pro	Gly	Gln	Gly	Ser	Gln	Arg	Lys	Lys	Arg	Ala	Leu	Asp	Thr	Asn	Asp		
	290					295				300							
tac	aag	gat	gac	gac	gac	aag	gcc	ctg	gac	acc	aat	tac	tgc	ttc	cgc	960	
Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Arg		
305				310				315							320		
aac	ctg	gag	gag	aac	tgc	tgt	gta	cgc	ccc	ctt	tat	att	gac	ttc	cgg	1008	
Asn	Leu	Glu	Glu	Asn	Cys	Cys	Val	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Arg		
				325				330						335			
cag	gat	cta	ggc	tgg	aaa	tgg	gtc	cac	gaa	cct	aag	ggg	tac	tat	gcc	1056	
Gln	Asp	Leu	Gly	Trp	Lys	Trp	Val	His	Glu	Pro	Lys	Gly	Tyr	Tyr	Ala		
		340					345						350				
aac	ttc	tgc	tca	ggc	cct	tgc	cca	tac	ctc	cgc	agc	gca	gac	aca	acc	1104	
Asn	Phe	Cys	Ser	Gly	Pro	Cys	Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr		
		355					360					365					
cat	agc	acg	gtg	ctt	gga	cta	tac	aac	acc	ctg	aac	cca	gag	gcg	tct	1152	
His	Ser	Thr	Val	Leu	Gly	Leu	Tyr	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser		
	370				375					380							
gcc	tcg	cca	tgc	tgc	gtc	ccc	cag	gac	ctg	gag	ccc	ctg	acc	atc	ttg	1200	
Ala	Ser	Pro	Cys	Cys	Val	Pro	Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu		
385				390				395						400			
tac	tat	gtg	ggc	aga	acc	ccc	aag	gtg	gag	cag	ctg	tcc	aac	atg	gtg	1248	
Tyr	Tyr	Val	Gly	Arg	Thr	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Val		
			405				410						415				
gtg	aag	tcg	tgt	aag	tgc	agc	tga									1272	
Val	Lys	Ser	Cys	Lys	Cys	Ser											
		420															

<210> 29
 <211> 423
 <212> PRT
 <213> Fusion

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 <222> (895)..(909)
 <223> Encodes amino acid residues 1-5 of TGF-beta3

 <220>
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 <222> (910)..(933)
 *<223> Encodes FLAG epitope tag

 <220>
 <221> misc_feature
 <222> (895)..(1272)
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Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1 5 10 15

Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
 245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
 260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
 275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp
 290 295 300

Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg
 305 310 315 320

Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg
 325 330 335

Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala
 340 345 350

Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr
 355 360 365

His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser
 370 375 380

Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu
 385 390 395 400

Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val
 405 410 415

Val Lys Ser Cys Lys Cys Ser
 420

<210> 30
 <211> 1284
 <212> DNA
 <213> Fusion

<220>
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<220>
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 1 5 10 15

aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac 96
 Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
 20 25 30

atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag 144
 Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
 35 40 45

ctc agg ctc acc agc ccc cct gag cca tcg gtg atg acc cac gtc ccc 192
 Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
 50 55 60

tat cag gtc ctg gca ctt tac aac agc acc cgg gag ttg ctg gaa gag 240
 Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
 65 70 75 80

atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tcg gag tct 288
 Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
 85 90 95

gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg 336
 Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
 100 105 110

gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag 384
 Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
 115 120 125

gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg 432
 Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
 130 135 140

ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag 480
 Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
 145 150 155 160

cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag 528
 Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
 165 170 175

cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg 180 185 190	576
ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu 195 200 205	624
tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Ile Ser Ile His 210 215 220	672
tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val 225 230 235 240	720
cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp 245 250 255	768
cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His 260 265 270	816
aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser 275 280 285	864
cca ggc cag ggc agt cag agg aag aag agg gcc ctg gac acc aat agc Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser 290 295 300	912
tac cca tac gac gtg cca gac tac gca tct ctg gcc ctg gac acc aat Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn 305 310 315 320	960
tac tgc ttc cgc aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr 325 330 335	1008
att gac ttc cgg cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys 340 345 350	1056
ggc tac tat gcc aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser 355 360 365	1104
gca gac aca acc cat agc acg gtg ctt gga cta tac aac acc ctg aac Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn 370 375 380	1152
cca gag gcg tct gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro 385 390 395 400	1200
ctg acc atc ttg tac tat gtg ggc aga acc ccc aag gtg gag cag ctg Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu 405 410 415	1248
tcc aac atg gtg gtg aag tcg tgt aag tgc agc tga	1284

Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
 420 425

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 <223> Encodes amino acid residues 1-5 of TGF-beta3

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Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
 20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
 35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
 50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
 65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
 85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
 100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
 115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
 130 135 140

Phe Arg Ala Glu Phe-Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser
290 295 300

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn
305 310 315 320

Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr
325 330 335

Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys
340 345 350

Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser
355 360 365

Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn
370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro
 385 390 395 400

Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu
 405 410 415

Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
 420 425

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<220>
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 <222> (860)..(883)
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 1 5 10

ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga 97
 Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
 15 20 25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc	145
Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg	
30 35 40 45	
atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc	193
Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser	
50 55 60	
ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta	241
Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val	
65 70 75	
ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc	289
Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val	
80 85 90	
gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc	337
Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr	
95 100 105	
cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag	385
Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys	
110 115 120 125	
ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg	433
Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg	
130 135 140	
gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg	481
Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu	
145 150 155	
ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa	529
Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys	
160 165 170	
tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc	577
Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro	
175 180 185	
agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg	625
Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg	
190 195 200 205	
cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc	673
Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala	
210 215 220	
cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac	721
His Ser Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn	
225 230 235	
ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg	769
Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met	
240 245 250	
aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag	817
Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln	
255 260 265	

cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac gac tac	865
His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr	
270 275 280 285	
aag gat gac gac gac aag gcc ctg gat acc aac tac tgc ttc agc tcc	913
Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser	
290 295 300	
acg gag aag aac tgc tgc gtg cgg cag ctc tac att gac ttc cgg aag	961
Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys	
305 310 315	
gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc tac cat gcc aat	1009
Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn	
320 325 330	
ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta gac act cag tac	1057
Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr	
335 340 345	
agc aag gtc ctg gct ctg tac aac cag cac aac ccg ggc gcg tcg gcg	1105
Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala	
350 355 360 365	
gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg ccc atc gtg tac	1153
Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr	
370 375 380	
tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc gtg	1201
Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val	
385 390 395	
cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc cccgcccacc	1252
Arg Ser Cys Lys Cys Ser	
400	
cggcaggccc ggccccaccc ccgcccgcct cacoggggct gtattttaagg acatcgtgcc	1312
ccaagcccac ttgggatcga ttaaagcggc cgcgact	1349

<210> 33
 <211> 403
 <212> PRT
 <213> Fusion

<220>
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 <222> (845)..(859)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (860)..(883)
 <223> Encodes FLAG epitope tag

<220>
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 <222> (845)..(1222)
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<400> 33

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
 275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
 355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 385 390 395 400

Lys Cys Ser

<210> 34
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 <212> DNA
 <213> Fusion

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 <222> (849)..(863)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (864)..(887)
 <223> Encodes FLAG epitope tage

<220>
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 <222> (849)..(1226)
 <223> Encodes mature fusion protein

<400> 34
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 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu
 1 5 10

ctg ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc 98
 Leu Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala
 15 20 25

gga ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag 146
 Gly Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys
 30 35 40

cgc atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc 194
 Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala
 45 50 55 60

agc ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca 242
 Ser Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala
 65 70 75

gta ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt 290
 Val Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser
 80 85 90

gtc gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc 338
 Val Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val
 95 100 105

acc cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc 386
 Thr Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe
 110 115 120

aag ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc 434
 Lys Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu
 125 130 135 140

tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc 1202
 Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
 385 390 395

gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc cccgcccacc 1256
 Val Arg Ser Cys Lys Cys Ser
 400

cggcaggccc ggccccaccc ccgcccgcct caccgggggt gtattttaagg acatcgtgcc 1316
 ccaagcccac ttgggatcga ttaaagcggc cgcgact 1353

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 <212> PRT
 <213> Fusion

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<220>
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 <223> Encodes FLAG epitope tage

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 <222> (849)..(1226)
 <223> Encodes mature fusion protein

<400> 35

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
 210 215 220

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
 225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
 275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
 355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 385 390 395 400

Lys Cys Ser

<210> 36
 <211> 1361
 <212> DNA
 <213> Fusion

<220>
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<220>
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<220>
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 <223> Encodes mature fusion protein

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49

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ccg	ctg	ctg	tgg	ctg	cta	gtg	ctg	acg	cct	ggc	cgg	ccg	gcc	gcc	gga			97
Pro	Leu	Leu	Trp	Leu	Leu	Val	Leu	Thr	Pro	Gly	Arg	Pro	Ala	Ala	Gly			
15			20			25												
ctg	tcc	acc	tgc	aag	acc	atc	gac	atg	gag	ctg	gtg	aag	cgg	aag	cgc			145
Leu	Ser	Thr	Cys	Lys	Thr	Ile	Asp	Met	Glu	Leu	Val	Lys	Arg	Lys	Arg			
30			35			40									45			
atc	gag	gcc	att	cgc	ggc	cag	att	ctg	tcc	aag	ctt	cgg	ctt	gcc	agc			193
Ile	Glu	Ala	Ile	Arg	Gly	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Ala	Ser			
			50			55									60			
ccc	ccg	agc	cag	ggg	gac	gtg	ccg	ccc	ggc	ccg	ctg	cct	gag	gca	gta			241
Pro	Pro	Ser	Gln	Gly	Asp	Val	Pro	Pro	Gly	Pro	Leu	Pro	Glu	Ala	Val			
			65			70									75			
ctg	gct	ctt	tac	aac	agt	acc	cgc	gac	cgg	gta	gcc	ggg	gaa	agt	gtc			289
Leu	Ala	Leu	Tyr	Asn	Ser	Thr	Arg	Asp	Arg	Val	Ala	Gly	Glu	Ser	Val			
80						85						90						
gaa	ccg	gag	ccc	gag	cca	gag	gcg	gac	tac	tac	gcc	aag	gag	gtc	acc			337
Glu	Pro	Glu	Pro	Glu	Pro	Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr			
95						100						105						
cgc	gtg	cta	atg	gtg	gaa	agc	ggc	aac	caa	atc	tat	gat	aaa	ttc	aag			385
Arg	Val	Leu	Met	Val	Glu	Ser	Gly	Asn	Gln	Ile	Tyr	Asp	Lys	Phe	Lys			
110			115			120									125			
ggc	acc	ccc	cac	agc	tta	tat	atg	ctg	ttc	aac	acg	tcg	gag	ctc	cgg			433
Gly	Thr	Pro	His	Ser	Leu	Tyr	Met	Leu	Phe	Asn	Thr	Ser	Glu	Leu	Arg			
			130			135									140			
gaa	gcg	gtg	ccg	gaa	cct	gta	ttg	ctc	tct	cgg	gca	gag	ctg	cgc	ctg			481
Glu	Ala	Val	Pro	Glu	Pro	Val	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu			
			145			150						155						
ctg	agg	ctc	aag	tta	aaa	gtg	gag	cag	cac	gtg	gag	cta	tac	cag	aaa			529
Leu	Arg	Leu	Lys	Leu	Lys	Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys			
160						165						170						
tac	agc	aat	gat	tcc	tgg	cgc	tac	ctc	agc	aac	cgg	ctg	ctg	gcc	ccc			577
Tyr	Ser	Asn	Asp	Ser	Trp	Arg	Tyr	Leu	Ser	Asn	Arg	Leu	Leu	Ala	Pro			
175						180						185						
agt	gac	tca	ccg	gag	tgg	ctg	tcc	ttt	gat	gtc	acc	gga	gtt	gtg	cgg			625
Ser	Asp	Ser	Pro	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg			
190			195			200						205						
cag	tgg	ctg	acc	cgc	aga	gag	gct	ata	gag	ggg	ttt	cgc	ctc	agt	gcc			673
Gln	Trp	Leu	Thr	Arg	Arg	Glu	Ala	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala			
			210			215						220						
cac	tct	tcc	tct	gac	agc	aaa	gat	aac	aca	ctc	cac	gtg	gaa	att	aac			721
His	Ser	Ser	Ser	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn			
			225			230						235						
ggg	ttc	aat	tct	ggc	cgc	cgg	ggg	gac	ctg	gcc	acc	att	cac	ggc	atg			769
Gly	Phe	Asn	Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met			
240						245						250						

aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag 817
 Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
 255 260 265

 cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac agc tac 865
 His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr
 270 275 280 285

 cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac 913
 Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr
 290 295 300

 tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att 961
 Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile
 305 310 315

 gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc 1009
 Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly
 320 325 330

 tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta 1057
 Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu
 335 340 345

 gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg 1105
 Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro
 350 355 360 365

 ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg 1153
 Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu
 370 375 380

 ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc 1201
 Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser
 385 390 395

 aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc 1254
 Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 400 405

 cccgccacc cggcaggccc ggccccaccc ccgcccgcct caccgggggt gtattttaagg 1314
 acatcgtgcc ccaagcccac ttgggatcga ttaaagcggc cgcgact 1361

<210> 37
 <211> 407
 <212> PRT
 <213> Fusion

<220>
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 <222> (845)..(859)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (860)..(895)
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<220>
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 <222> (845)..(1234)
 <223> Encodes mature fusion protein

<400> 37

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
 210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
405

<210> 38
<211> 1361
<212> DNA
<213> Fusion

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<220>
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 <223> Encodes HA epitope tag

<220>
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 <222> (845)..(1234)
 <223> Encodes mature fusion protein

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 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
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 ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga 97
 Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
 15 20 25

 ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc 145
 Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
 30 35 40 45

 atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc 193
 Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
 50 55 60

 ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta 241
 Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
 65 70 75

 ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc 289
 Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
 80 85 90

 gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc 337
 Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
 95 100 105

 cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag 385
 Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys

110	115	120	125	
ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg 130 135 140				433
gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu 145 150 155				481
ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys 160 165 170				529
tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro 175 180 185				577
agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg 190 195 200 205				625
cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala 210 215 220				673
cac tgt tcc tgt gac agc aaa gat aac aca ctc cac gtg gaa att aac His Cys Ser Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn 225 230 235				721
ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met 240 245 250				769
aac cgg ccc ttc ctg ctc ctc atg gcc acc cgg ctg gag agg gcc cag Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln 255 260 265				817
cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac agc tac His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr 270 275 280 285				865
cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr 290 295 300				913
tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile 305 310 315				961
gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly 320 325 330				1009
tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu 335 340 345				1057
gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro 350 355 360 365				1105

ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg 1153
 Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu
 370 375 380

ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc 1201
 Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser
 385 390 395

aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc 1254
 Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 400 405

cccgcccacc cggcaggccc ggccccaccc ccgcccgcct caccgggggt gtattttaagg 1314

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 <223> Encodes amino acid residues 1-5 of TGF-beta1

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 <223> Encodes HA epitope tag

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 <223> Encodes mature fusion protein

<400> 39

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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
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Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu

85

90

95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
405